

Sequence Listing

<110> Baker, Kevin
Botstein;David
Eaton, Dan
Ferrara,Napoleone
Filvaroff,Ellen
Gerritsen,Mary
Goddard,Audrey
Godowski,Paul
Grimaldi,Christopher
Gurney,Austin
Hillan,Kenneth
Kljavin,Ivar
Napier,Mary
Roy,Margaret
Tumas,Daniel
Wood,William

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Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
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140 145 150
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170 175 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 190 195
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260 265 270
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tttattggtt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000
cttaactctg gtggtaagg tcagcacctg tgcggccgggg gagagtcacg 1050

caa atgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100
gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150
tgaagaatac gatgcttgc agaggaaacc ttgccaaaac aacgcgagct 1200
gtattgatgc aaatgaaaag caagatggaa gcaatttcac ctgtgttgc 1250
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tcacactgcca gtgtccagaa ggatacttcg gatctgtttt tgaagaaaag 1400
gtggacccct ggcgcctcg tcgcgtccag aacaacggca cctgctatgt 1450
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cctgtgcccac gcttatttgc ttctgtgccc tcagccctgt tgctcatggc 1550
acgtgccgca gctgtggcact cagctacaaa tgcgtctgtt atccagggtt 1600
ccatggccctc tactgtgagg aggaatataa tgagtgcctc tccgcctccat 1650
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cgctaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800
atggcacgtg catctgtgca cccgggttta caggtgaaga gtgcgcacatt 1850
gacataaaatg aatgtgacag taacccctgc caccatgggtt ggagctgcct 1900
ggaccagccc aatggttata actgccactg cccgcattgtt tgggtggag 1950
caaactgtga gatccacactc caatggaaatg ccgggcacat ggccggagagc 2000
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ccggcatgccc aggtttggaa agaaatcccg gcctgcaatgt tatgtatgtga 2250
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gatgagatac tacactcatt taaatatttt taagaaaata aaaagcttaa 2400
gaaatttaaa atgcttagctg ctcaagagttt ttcagttagaa tatttaagaa 2450
ctaattttctt gcagctttta gtttggaaaaa aatattttaa aaacaaaattt 2500

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ttctttaaaa agtcaagggt tctatattgtt gagaattttaa aatttacattt 3050
tgagttgtttt gttgctaaga ggtagtaaat gtaagagagt actggttcct 3100
tcagtagtga gtatttctca tagtgcagct ttatttatctt ccaggatgtt 3150
tttggctg tatttgatttgc atatgtgtttt cttctgatttcc ttgctaattt 3200
ccaaccatata tgaataaaatg tgaatcaagtc a 3231

<210> 15
<211> 737
<212> PRT
<213> Homo Sapien

<400> 15
Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro
1 5 10 15
Ala Leu Ala Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly
20 25 30
Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
35 40 45
Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60
Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
65 70 75
Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
80 85 90
Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
95 100 105
Gly Asn Cys Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly	Lys Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

Thr Cys Ile Ser Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu
 410 415 420
 Gly Tyr Phe Gly Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala
 425 430 435
 Ser Ser Pro Cys Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val
 440 445 450
 His Phe Thr Cys Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys
 455 460 465
 Ala Gln Leu Ile Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly
 470 475 480
 Thr Cys Arg Ser Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro
 485 490 495
 Gly Tyr His Gly Leu Tyr Cys Glu Glu Tyr Asn Glu Cys Leu
 500 505 510
 Ser Ala Pro Cys Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn
 515 520 525
 Gly Tyr Glu Cys Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys
 530 535 540
 Glu Leu Tyr Lys Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly
 545 550 555
 Ala Thr Cys Asp Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala
 560 565 570
 Pro Gly Phe Thr Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys
 575 580 585
 Asp Ser Asn Pro Cys His His Gly Ser Cys Leu Asp Gln Pro
 590 595 600
 Asn Gly Tyr Asn Cys His Cys Pro His Gly Trp Val Gly Ala Asn
 605 610 615
 Cys Glu Ile His Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser
 620 625 630
 Leu Thr Asn Met Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala
 635 640 645
 Leu Cys Val Ala Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly
 650 655 660
 Ile Cys Arg Ile Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro
 665 670 675
 Ala Tyr Glu Glu Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe
 680 685 690
 Ser Asn Ala Ile Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
725 730 735

Asp Leu

<210> 16
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 16
tgtaaaaacga cggccagttt aatagacctg caattattaa tct 43

<210> 17
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 17
cagggaaacag ctaggaccac ctgcacaccc gcaaattccat t 41

<210> 18
<211> 508
<212> DNA
<213> Homo Sapien

<400> 18
ctctggaagg tcacggccac aggattccaa cagtgcctcc tcatacatgg 50
acgaaaagtgt gaccccccctt tcaggcttcc agggggactg gtccctcctgg 100
aggagatgtc cgccttgggg aataatcaact ttattgggtt tgtgaatgtat 150
tcttgacta agtctattgt ggcttgcgc ttaactctgg tggtaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttccctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gagggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatgggag caatttcacc tgtgtttgcc ttccctggta tactggagag 450
ctttgccaac cgaactgaga ttggagcgtaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 19
ctctggaagg tcacggccac aggattccaa cagtgcctcc tcatacatgg 50
acgaaaagtgt gaccccccctt tcaggcttcc agggggactg gtcctctgg 100
aggagatgct cgccttgggg aataatcaact ttattggttt tgtgaatgat 150
tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggtaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gagggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatgggag caatttcacc tgtgttgcc ttccctggta tactggagag 450
ctttgccaac cgaactgaga ttggagcga cgacctacac cgaactgaga 500
taggggag 508

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
ctctggaagg tcacggccac agg 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaagc tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgcctcc tcatacatgg acgaaagtgt gaccccccctt tcaggcgaga 50
gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagtcgt ctgctcctgc tgctgctgct ccagcctgta acctgtgcct 50
acaccacgccc agggccccc agagccctca ccacgctggg cgcccccaga 100
gcccacacca tgccgggacac ctacgctccc tcgaccacac tcagtagtcc 150
cagcacccag ggcctgcaag agcaggcacg ggccctgatg cgggacttcc 200
cgctcggtga cggccacaac gacctgcccc tggtcctaag gcaggtttac 250
cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300
cagcctggac aggcttagag atggcctcggt gggcgcccag ttctggtcag 350
cctatgtgcc atgccagacc caggaccggg atgccctgcg cctcaccctg 400
gagcagattg acctcatacg ccgcattgtgt gcctcctatt ctgagctgga 450
gcttgcgtacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500
tcatcggtgt agagggtggc cactcgctgg acaatagct ctccatctta 550
cgtaccttct acatgctggg agtgcgcctac ctgacgctca cccacacctg 600
caacacaccc tgggcagaga gctccgctaa gggcgccac tccttctaca 650
acaacatcag cgggctgact gactttgggt agaagggtggt ggcagaaatg 700
aaccgcctgg gcatgatggc agacttatcc catgtctcag atgctgtggc 750
acggcgggccc ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800
ctgcccgggg tgtgtgcaac agtgcgtggc atgttcctga tgacatcctg 850
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agtaatacag tgcaacccat cagccatgt gtccactgtg gcagatcact 950
tcgaccacat caaggctgtc attggatcca agttcatcgg gattgggtgg 1000
gattatgatg gggccggcaa attccctcag gggctggaaag acgtgtccac 1050
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agttcaggg tgtccttcgt ggaaacctgc tgcgggtt cagacaagtg 1150

gaaaaggtac aggaagaaaa caaatggcaa agccccttgg aggacaagtt 1200
cccgatgag cagctgagca gttcctgcca ctccgacctc tcacgtctgc 1250
gtcagagaca gagtctgact tcaggccagg aactcaactga gattccata 1300
caactggacag ccaagttacc agccaagtgg tcagtctcag agtcctcccc 1350
ccacatggcc ccagtcccttg cagttgtggc caccttccca gtccttattc 1400
tgtggctctg atgaccctagt tagtcctgcc agatgtcaact gtagcaagcc 1450
acagacaccc cacaaagttc ccctgttgtc caggcacaaa tatttcctga 1500
aataaatgtt ttggacatag 1520

<210> 24
<211> 433
<212> PRT
<213> Homo Sapien

<400> 24
Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
1 5 10 15
Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser
50 55 60
Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
65 70 75
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
95 100 105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
 185 190 195
 Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
 200 205 210
 Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
 215 220 225
 Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
 230 235 240
 Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly
 245 250 255
 Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
 260 265 270
 Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
 275 280 285
 Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
 290 295 300
 Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
 305 310 315
 Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
 320 325 330
 Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
 335 340 345
 Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
 350 355 360
 Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
 365 370 375
 Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
 380 385 390
 Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
 395 400 405
 Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu
 410 415 420
 Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu
 425 430

<210> 25
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggtg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatacg ccgcattgtgt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50
gatccgcggc cgcaattct aaaccaacat gcccggcacc tacgctccct 100
cgaccacact cagtagtccc agcacccagg gcctgcaaga gcaggcacgg 150
gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200
ggtcctaagg caggttacc agaaaggct acaggatgtt aacctgcgca 250
atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350
tgcctgcgc ctcacccctgg agcagattga cctcatacgc cgcatgtgtg 400

cctccatttc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450
actcagaaat tggcctgcct catcggtgta gagggtggcc actcgctgga 500
caatagcctc tccatcttac gtaccttcta catgctggga gtgcgcctacc 550
tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600
ggcgtccact cttctacaa caacatcagc gggctgactg actttggta 650
gaaggtggtg gcagaaatga accgcctggg catgatgta gacttatccc 700
atgtctcaga tgctgtggca cggcgcccc tggaaagtgtc acaggcacct 750
gtgatcttct cccactcggc tgcccggtgt gtgtgcaaca gtgctcgaa 800
tgttcctgat gacatcctgc agctctgaa gaagaacggt ggcgtcgtga 850
tgggtcttt gtccatggga gtaatacagt gcaacccatc agccaatgtg 900
tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatccaa 950
gttcatcgaa attgggtggag attatgatgg ggccggcaaa ttccctcagg 1000
ggctggaaga cgtgtccaca taccgggtcc tgatagagga gttgctgagt 1050
cgtggctgga gtgaggaaga gcttcagggt gtccttcgtg gaaacctgct 1100
gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaac aaatggcaaa 1150
gccccttggaa ggacaagttc ccggatgagc agctgagcag ttccctgccac 1200
tccgacctct cacgtctgcg tcagagacag agtctgactt cagggccagga 1250
actcactgag attcccatac actggacagc caagttacca gccaagtgg 1300
cagtcctcaga gtcctcccc caccctgaca aaactcacac atgcccaccc 1350
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc 1400
aaaacccaag gacacc 1416

<210> 30
<211> 446
<212> PRT
<213> Homo Sapien

<400> 30
Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
1 5 10 15
Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

50	55	60
Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly		
65	70	75
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg		
80	85	90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg		
95	100	105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys		
110	115	120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu		
125	130	135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe		
140	145	150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn		
155	160	165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr		
170	175	180
Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala		
185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser		
200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val		
215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg		
230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly		
245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro		
260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys		
275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp		
290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu		
320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
335	340	345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
 350 355 360
 Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
 365 370 375
 Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
 380 385 390
 Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
 395 400 405
 Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
 410 415 420
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 425 430 435
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 440 445

<210> 31
 <211> 1790
 <212> DNA
 <213> Homo Sapien

<400> 31
 cggccagcga cgtgcgggcg gcctggcccg cgccctcccg cgcccgccct 50
 gcgtcccccgccg ccctgcgcaca ccggccgcga gccgcagccc gccgcgcgc 100
 cccggcagcgc ccggccccat gcccgcggc cgccggggcc ccggccgcaca 150
 atccgcgcgg cggccgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
 tcctcggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250
 ccccaggatc ccacgcttct catggctcc tccctgctgg ccacctgctc 300
 agtgcacgga gacccaccag gagccaccgc cgagggcctc tactggaccc 350
 tcaacgggcg ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400
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 gcctctatgt tggccctgccc ccagagaaac ccgtcaacat cagctgctgg 550
 tccaagaaca tgaaggactt gacctgccgc tggacgccag gggcccacgg 600
 ggagaccttc ctccacacca actactccct caagtacaag ctttaggtgg 650
 atggccagga caacacatgt gaggagtacc acacagtggg gccccactcc 700
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<210> 32
<211> 422
<212> PRT
<213> Homo Sapien

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<400> 32
Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
      1           5           10          15

Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Cys Val Leu Gly
      20          25          30

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
      35          40          45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
      50          55          60

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Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr
 65 70 75
 Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val
 80 85 90
 Leu Asn Ala Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly
 95 100 105
 Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
 110 115 120
 Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro
 125 130 135
 Glu Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp
 140 145 150
 Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu
 155 160 165
 His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln
 170 175 180
 Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His Ser Cys
 185 190 195
 His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp
 200 205 210
 Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
 215 220 225
 Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp
 230 235 240
 Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
 245 250 255
 Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala
 260 265 270
 Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
 290 295 300
 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro
 305 310 315
 Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp
 320 325 330
 Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly
 335 340 345
 Pro Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser

350 355 360
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys
365 370 375
Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln
380 385 390
Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp
395 400 405
Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro
410 415 420
Ala Arg

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
cccgcccgac gtgcacgtga gcc 23

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
tgagccagcc caggaactgc ttg 23

<210> 35
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
caagtgcgct gcaaccctt tggcatctat ggctccaaga aagccggat 50

<210> 36
<211> 1771
<212> DNA
<213> Homo Sapien

<400> 36
cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacacccaaa cgctcgacgc cacaagg 100
atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgctg 150
ctccctagag tccttcgtga agcttttat tcctaagagg agaaaatcag 200
tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250
ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350
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gcacaggaa gctagaggtg gatacacgtg ttgcaagttaaaagcatca 1600
ctgggattta aggagaatttggagaaatgttgcataatgcagcaataa 1650
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aaaaaaaaaaa aaaaaaaaaaaa a 1771

<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37
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Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45
His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
50 55 60
Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
65 70 75
Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
80 85 90
Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
95 100 105
Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
110 115 120
Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
125 130 135
Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
140 145 150
Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
155 160 165
His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
170 175 180
Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195
His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly

200 205 210

Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe
215 220 225

Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys
245 250 255

Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu
260 265 270

Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
275 280 285

Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggtaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagcctgtt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

gctggtag tctatacatac agattttttt gctacacaag atccctcag 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien

<400> 41
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gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
ccgaaggagg ccatcgggga gccgggaggg gggactgcga gaggaccccg 200
gcgtccgggc tcccggtgcc agcgctatga ggccactcct cgtcctgctg 250
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cagcctctgc ccggggcacc ccggccttcc aggacacgccc ggccaccatg 350
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cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgccggg 450
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aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1377

<210> 42

<211> 243
<212> PRT
<213> Homo Sapien

<400> 42

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	20						25					30		
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly
	35						40				45			
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly
	50						55				60			
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly
	65						70				75			
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly
	80						85				90			
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala
	95						100				105			
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp
	110						115				120			
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His
	125						130				135			
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val
	140						145				150			
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln
	155						160				165			
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln
	170						175				180			
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala
	185						190				195			
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly
	200						205				210			
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser
	215						220				225			
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro
	230						235				240			
Val	Phe	Ala												

<210> 43
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
tacaggccca gtcaggacca gggg 24

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
agccagcctc gctctcg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtctgcgtac aggtctgg 18

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
gaaagaggca atggattcgc 20

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
gacttacact tgccagcaca gcac 24

<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49
<211> 1876
<212> DNA
<213> Homo Sapien

<400> 49
ctctttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccattgtcga tccagagacc tccctggcc 150
gggggcatct cctggctgtg ctccctggccc tccttggcac cacctggca 200
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tatgaatcag ctgaaaaaaaaaaaaa 1876

<210> 50
<211> 455
<212> PRT
<213> Homo Sapien

<400> 50
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1 5 10 15
Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
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Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
35 40 45
Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
50 55 60
Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
65 70 75
Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
80 85 90
Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
95 100 105
Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala Glu Gly Gln Arg Tyr Ser		
125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn Ala Thr Cys Thr His Tyr		
140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser Gln Leu Gly Cys Gly Arg		
155	160	165
His Leu Cys Ser Ala Gly Gln Thr Ala Ile Glu Ala Phe Val Cys		
170	175	180
Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly Lys Thr Ile		
185	190	195
Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr Ala Ser		
200	205	210
Val Ser Gly Cys Phe Lys Ala Trp Asp His Ala Gly Gly Leu Cys		
215	220	225
Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly		
230	235	240
Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr		
245	250	255
Thr Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His		
260	265	270
Gly Arg Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly		
275	280	285
Tyr Gly Gly Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His		
290	295	300
Thr Cys Asp Leu Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser		
305	310	315
Glu Ala Asp Thr Tyr Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys		
320	325	330
Gly Gly Val Leu Ala Gln Ile Lys Ser Gln Lys Val Gln Asp Ile		
335	340	345
Leu Ala Phe Tyr Leu Gly Arg Leu Glu Thr Thr Asn Glu Val Thr		
350	355	360
Asp Ser Asp Phe Glu Thr Arg Asn Phe Trp Ile Gly Leu Thr Tyr		
365	370	375
Lys Thr Ala Lys Asp Ser Phe Arg Trp Ala Thr Gly Glu His Gln		
380	385	390
Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro Asp Asn His Gly Leu		
395	400	405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420
Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435
Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450
Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttccgctg ggccacaggg gagcaccagg ctttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
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ttcatcacca acttcactat gcttatttggaa gacaagggtgt atcagggcga 400
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gatgtgcctg tgccgcctca gaaggcaggg aaagatgtca caggaagccc 1750
caggecttga ggcgatggag agggggacac caaccacatc gagcgtctct 1800
ggagctacct caccacaaag gagctgtga gctctggct gcaaagtgac 1850
gatgaaccgg agaaggagcg gctgcggcag cggggcccagg ccctggctgt 1900
gagctaccgc ttccctcaccc cttcaccc catgaagctg agggggccgg 1950
tccccacgcat ggtggcctg gaggaggccc acggcatgtc ggctgccatg 2000
ggacccgaac cgggtgtgca gagcgtgcga ggagctggca cgcagccagg 2050
acctttgctc aagaagccaa actccgtcaa aaaaaaaca aacaaaacaa 2100
aaaaaaagaca tggagagat ggtgttttc ctctccacca cctgggata 2150
cgatgagaag atggccacct gcaagccagg aagacggccc tcaccagaca 2200
ccatgtctgc tggcacctg atcttgacc tccccacgctc cagaactgtg 2250
agaaataaat gtgtttgtt taagctaaaa aaaaaaaaaa aaaaaaaaaa 2300
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<210> 55
<211> 694
<212> PRT
<213> Homo Sapien

<400> 55
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35 40 45
Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile
50 55 60
Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn
65 70 75
Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro
80 85 90
Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys
95 100 105
Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
110 115 120

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu
 125 130 135
 Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys
 140 145 150
 Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg
 155 160 165
 Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln
 170 175 180
 Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala
 185 190 195
 Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln
 200 205 210
 Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser
 215 220 225
 Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
 230 235 240
 Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu
 245 250 255
 Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile
 260 265 270
 Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala
 275 280 285
 Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu
 290 295 300
 Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys
 305 310 315
 Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg
 320 325 330
 Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp
 335 340 345
 His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val
 350 355 360
 Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly
 365 370 375
 Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His
 380 385 390
 Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr
 395 400 405
 Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
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Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcat tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaaggacc acttgatatac agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
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ccagtgtgcg gcggcagcgg cggcgccggc gcctcccggg ctccggcttc 100
tgctgttgct cttctccggcc gcggcactga tccccacagg ttagtggcag 150
aatctgttta cgaaagacgt gacagtgtac gagggagagg ttgcgaccat 200

<210> 61
<211> 440
<212> PRT
<213> Homo Sapien

<400> 61
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20					25					30				
Phe	Ser	Ala	Ala	Ala	Leu	Ile	Pro	Thr	Gly	Asp	Gly	Gln	Asn	Leu
35					40					45				
Phe	Thr	Lys	Asp	Val	Thr	Val	Ile	Glu	Gly	Glu	Val	Ala	Thr	Ile
50					55					60				
Ser	Cys	Gln	Val	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu
65					70					75				
Asn	Pro	Asn	Arg	Gln	Thr	Ile	Tyr	Phe	Arg	Asp	Phe	Arg	Pro	Leu
80					85					90				
Lys	Asp	Ser	Arg	Phe	Gln	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu
95					100					105				
Lys	Val	Ser	Leu	Thr	Asn	Val	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr
110					115					120				
Phe	Cys	Gln	Leu	Tyr	Thr	Asp	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	Thr
125					130					135				
Ile	Thr	Val	Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Ile	Asp	Ile	Gln
140					145					150				
Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr
155					160					165				
Ala	Met	Ala	Ser	Lys	Pro	Ala	Thr	Thr	Ile	Arg	Trp	Phe	Lys	Gly
170					175					180				
Asn	Thr	Glu	Leu	Lys	Gly	Lys	Ser	Glu	Val	Glu	Glu	Trp	Ser	Asp
185					190					195				
Met	Tyr	Thr	Val	Thr	Ser	Gln	Leu	Met	Leu	Lys	Val	His	Lys	Glu
200					205					210				
Asp	Asp	Gly	Val	Pro	Val	Ile	Cys	Gln	Val	Glu	His	Pro	Ala	Val
215					220					225				
Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	Leu	Glu	Val	Gln	Tyr	Lys
230					235					240				
Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	Leu	Gln	Gly	Leu	Thr
245					250					255				
Arg	Glu	Gly	Asp	Ala	Leu	Glu	Leu	Thr	Cys	Glu	Ala	Ile	Gly	Lys
260					265					270				
Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met
275					280					285				
Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn
290					295					300				
Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn														

305 310 315

Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
320 325 330

Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr
335 340 345

Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg
350 355 360

Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile
365 370 375

Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu
380 385 390

Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe
395 400 405

Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr
410 415 420

Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys
425 430 435

Lys Glu Tyr Phe Ile
440

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

ggcttctgct gttgctcttc tccg 24

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gtacactgtg accagtcagc 20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
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<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgccggcactg atccccacag gtgatggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcgggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50
cctcgggccc gacccgcacag gaaagactga ggccgcggcc tgccccgccc 100
ggctccctgc gccgcccgcg cctcccgggc cagaagatgt gctccagggt 150
ccctctgctg ctggcgctgc tcctgtact ggccctgggg cctggggtgc 200
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250
actgccccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggc 300
ggggctgtac gtcttgaga acggcatcac catgctcgac gcaaggcagct 350
ttggccggcct gccgggcctg cagctcctgg acctgtcaca gaaccagatc 400

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aaaaaa 2555

<210> 69
<211> 598
<212> PRT
<213> Homo Sapien

<400> 69
Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu
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Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
20 25 30
Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
35 40 45
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
50 55 60
Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
65 70 75
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
80 85 90
Leu Arg Leu Pro Arg Leu Leu Leu Asp Leu Ser His Asn Ser
95 100 105
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

110	115	120
Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly		
125	130	135
Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp		
140	145	150
Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly		
155	160	165
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu		
170	175	180
Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp		
185	190	195
Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly		
200	205	210
Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe		
215	220	225
Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu		
230	235	240
Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe		
245	250	255
Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala		
260	265	270
Asp Phe Gly Cys Pro Ala Thr Thr Thr Ala Thr Val Pro Thr		
275	280	285
Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu		
290	295	300
Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro		
305	310	315
Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln		
320	325	330
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys		
335	340	345
His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly		
350	355	360
Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg		
365	370	375
Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr		
380	385	390
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu		
395	400	405

Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
410 415 420
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
425 430 435
Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
440 445 450
Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
455 460 465
Gly Arg Val Pro Glu Gly Glu Ala Cys Gly Glu Ala His Thr
470 475 480
Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
485 490 495
Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
500 505 510
Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg
515 520 525
Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
530 535 540
Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
545 550 555
Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Glu Ala Leu
560 565 570
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly
575 580 585
Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile
590 595

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ccctccactg cccccaccgac tg 22

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgtaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccaccc tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgccctaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcacttagga caaccttctt cccttctgca ccactgccc 50
cgcccccgc 100
gggtccccag 150
ggcctccagg 200
gcccctgtt 250
ggctctgt 300
gcccggctgca 350
tggcagagtc 400

tggggagaga tcccgaaaa ggagagcagt gtcacccaa aaacagaaga 450
agcagcactc tgtcctgcac ctggttccca ttaacgccac ctccaaggat 500
gactccgatg tgacagaggt gatgtggcaa ccagctctt ggcgtggag 550
aggcctacag gcccaaggat atggtgtccg aatccaggat gctggagttt 600
atctgctgta tagccaggtc ctgttcaag acgtgactt caccatgggt 650
caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700
tataagaagt atgcctccc acccgacccg ggcctacaac agctgctata 750
gcgcaggtgt ctccatcca caccaagggg atattctgag tgtcataatt 800
ccccgggcaa gggcgaaact taacctctct ccacatggaa cttccctggg 850
gtttgtgaaa ctgtgattgt gttataaaaa gtggctccca gcttggaaaga 900
ccaggggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
agggaatgtg caggaacaga ggcatttcc tgggtttggc tccccgttcc 1000
tcactttcc ctttcattc ccacccctta gactttgatt ttacggatat 1050
cttgcttctg ttccccatgg agctccg 1077

<210> 76
<211> 250
<212> PRT
<213> Homo Sapien

<400> 76
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
1 5 10 15
Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
20 25 30
Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
35 40 45
Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
50 55 60
Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
65 70 75
Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
80 85 90
Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
95 100 105
Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
110 115 120

Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
125 130 135
Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala
140 145 150
Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu
155 160 165
Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
170 175 180
Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg
185 190 195
Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
200 205 210
Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
215 220 225
Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
230 235 240
His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 77
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 77
cactttctcc ctcttcttcc ttactttcga gaaaccgcgc ttccgcttct 50
ggtcgcagag acctcggaga cccgcgcggg gagacggagg tgctgtgggt 100
gggggggacc tgtggctgct cgtaccgcgc cccaccctcc tcttctgcac 150
tgcgcgtccctc cggaaagaccc tttccccctgc tctgtttccct tcaccgagtc 200
tgtgcatcgc cccggacccgt gcccggagga ggcttggcccg gccccggcag 250
ctcttaggggc ggcgcgggag gagcggccgg cgggacggagg ggcggcccg 300
gaagatgggc tcccgtggac agggactctt gctggcgtac tgcctgctcc 350
ttgcctttgc ctctggcctg gtcctgagtc gtgtgcggccca tgtccagggg 400
gaacacggagg agtggggaggg gactgaggag ctgcgcgtcgc ctccggacca 450
tgcccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500
aggggctccc tgcttcccg gtcctgctgct gctgtgaccc cggtaacctcc 550
atgtacccgg cgaccgcgcgt gccccagatc aacatcacta tcttgaaagg 600
ggagaagggt gaccgcggag atcgaggcct ccaaggaaaa tatggcaaaa 650

caggctcagc aggggccagg ggccacactg gacccaaagg gcagaaggc 700
tccatggggg cccctgggg acggtgcaag agccactacg ccgcctttc 750
ggtggccgg aagaagccca tgcacagcaa ccactactac cagacggta 800
tcttcgacac ggagttcgtg aacctctacg accactcaa catgttcacc 850
ggcaagttct actgctacgt gcccgccctc tacttctca gcctcaacgt 900
gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950
aggaggttgt gatcttgttc ggcagggtgg ggcaccgcag catcatgcaa 1000
agccagagcc tgcgttgaa gctgcgagag caggaccagg tgtgggtacg 1050
cctctacaag ggcgaacgtg agaacgcctt cttcagcgag gagctggaca 1100
cctacatcac cttcagtggc tacctggta agcacgcac cgagccctag 1150
ctggccggcc acctccttcc ctctgccac cttccacccc tgcgtgtgc 1200
tgacccacc gcctttccc cgatccctgg actccgactc cctggctttg 1250
gcattcagtg agacgcctg cacacacaga aagccaaagc gatcggtgt 1300
cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350
ggcggggcac ccgcgagaac cctctggac cttccgggc cctctctgca 1400
cacatcctca agtgaccccg cacggcgaga cgcgggtggc ggcagggcgt 1450
cccagggtgc ggcacccggg ctccagtcct tggaaataat taggcaaatt 1500
ctaaaggctt caaaaggagc aaagtaaacc gtggaggaca aagaaaagg 1550
ttgttatttt tgcgtttcca gccagcctgc tggctccaa gagagaggcc 1600
tttcagttt agactctgtt taagagaaga tccaaagtta aagctctggg 1650
gtcaggggag gggccggggg cagggaaacta cctctggctt aattctttt 1700
agccacgtag gaactttttt gaggatagg tggaccctga catccctgtg 1750
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ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgagggcag 1950
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ctgttttta taaaacacct caagcagcac tgca~~gt~~tc~~cc~~ catctc~~ctcg~~ 2150
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ccctgccc~~at~~ ggccacccca gactctgatc tccaggaacc ccata~~g~~cccc 2550
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ggcccccaaa cccccc~~gt~~gc tctctt~~cc~~ tccccccatc ccccacctgg 2650
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tccctaagtc cctctctt~~ta~~ aagaacttct gcgggtcaga ctctgaagcc 2750
gagttgctgt gggcgtcccc ggaagcagag c~~g~~ccacactc gctgcttaag 2800
ctccccc~~ag~~c tcttccaga aaacattaaa ctcagaatt~~g~~ tg~~ttt~~caa 2849

<210> 78
<211> 281
<212> PRT
<213> Homo Sapien

<400> 78
Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
1 5 10 15
Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
20 25 30
Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
35 40 45
Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
50 55 60
Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
65 70 75
Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
80 85 90
Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
95 100 105
Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

<210> 79
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 79
 tacaggccca gtcaggacca gggg 24

 <210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 80
 ctgaagaagt agaggccggg cacg 24

 <210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccggtgctt gcgctgtgt gaccccgta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gcggagcatc cgctgcggc ctcgccgaga ccccccgcg gattcgcgg 50
tccttcccgc gggcgcgaca gagctgtctt cgcacctgga tggcagcagg 100
ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcago 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaact aaactgaaat taaaaatgtt cttcggggaa gaaggagct 250
tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300
agtcaagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
gtcatctctt tctaaggaa tcagaggcaa tgagccgta tatacttcaa 400
ctcaagaaga ctgcattaaat tctgtgttt caacaaaaaa catatcaggg 450
gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
acccaactgc tacctatttt tctgtccaa cgaggaagcc tgtccattga 550
aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
ttgaccagaa atttgccaag ccaagagttt cccaggaag attctctctt 650
acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700
attattcaaa gcccaccgat atctcatgga gagacacact ttctcagaag 750
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tgcccagctc cttgcttata agggaaaaagg ccattctcag agttcacaat 850
tttctctga tcaagaaata gctcatctgc tgccctgaaaa tgtgagtgcg 900
ctcccagcta cggtggcagt tgcttctcca cataccacct cggctactcc 950
aaagcccccc acccttctac ccaccaatgc ttcagtgaca cttctggaa 1000
cttccccagcc acagctggcc accacagctc cacctgttaac cactgtcact 1050

tctcaggcctc ccacgaccct catttctaca gtttttacac gggctgcggc 1100
tacactccaa gcaatggcta caacagcagt tctgactacc acctttcagg 1150
cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaaatc 1200
tccaaacttaa ctttgaacac agggaatgtg tataacccta ctgcactttc 1250
tatgtcaaat gtggagtctt ccactatgaa taaaactgtt tcctggaaag 1300
gtagggaggc cagtccaggc agttcctccc agggcagtgt tccagaaaat 1350
cagtaacggcc ttccatggta aaaatggctt cttatcggtt ccctgctt 1400
tgggtgtctg ttcttggtga taggcctcgt cctcctgggt agaattcctt 1450
cggaatcaact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500
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tagcacgatc tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750
ttctcctgcc tcagcctcct aagtatctgg gattacaggc atgtgccacc 1800
acacctgggt gattttgta ttttagtag agacggggtt tcaccatgtt 1850
ggtcaggctg gtctcaaact cctgacctag tgatccaccc tcctcggct 1900
cccaaagtgc tgggattaca ggcattgagcc accacagctg gcccccttct 1950
gttttatgtt tgggttttga gaaggaatga agtgggaacc aaatttaggtt 2000
attttggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050
aaagtaataa agtataattt ccatataat ttcaaaattt aactggcttt 2100
tatgcaaaga aacaggttag gacatctagg ttccaaattca ttccacattct 2150
tggttccaga taaaatcaac tgtttatatac aatttctaattt ggatttgctt 2200
ttcttttat atggattcct taaaactta ttccagatgt agttccttcc 2250
aattaaatat ttgaataaaat cttttgttac tcaa 2284

<210> 83
<211> 431
<212> PRT
<213> Homo Sapien

<400> 83
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile
1 5 10 15

Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu
 20 25 30
 Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
 35 40 45
 Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
 50 55 60
 Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
 65 70 75
 Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
 80 85 90
 Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
 95 100 105
 Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
 110 115 120
 Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
 125 130 135
 Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
 140 145 150
 Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
 155 160 165
 Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
 170 175 180
 His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
 185 190 195
 Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
 200 205 210
 Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
 215 220 225
 Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
 230 235 240
 Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
 245 250 255
 Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
 260 265 270
 Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
 275 280 285
 Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
 290 295 300
 Ala Val Leu Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly

305 310 315
Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
320 325 330
Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
335 340 345
Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
350 355 360
Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
365 370 375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
380 385 390
Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
395 400 405
Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
410 415 420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
425 430

<210> 84

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 84

agggaggatt atccttgacc tttgaagacc 30

<210> 85

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 85

gaagcaagtg cccagctc 18

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 86

cgggtccctg ctctttgg 18

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
caccgtagct gggagcgcac tcac 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
agtgttaagtc aagotccc 18

<210> 89
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
gcttcctgac actaaggctg tctgttagtc agaattgcct caaaaagag 49

<210> 90
<211> 957
<212> DNA
<213> Homo Sapien

<400> 90
cctggaagat gcgcccattg gctggtgcc tgctcaaggt ggtgttcgtg 50
gtcttcgcct ccttgtgtgc ctggattcg gggtacctgc tcgcagagct 100
cattccagat gcacccctgt ccagtgctgc ctatagcatac cgccgcatacg 150
gggagaggcc tgtcctcaaa gctccagtcc ccaaaaggca aaaatgtgac 200
caactggactc cctgcccattc tgacacctat gcctacaggt tactcagcgg 250
agggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacctactta 300
tgggagaaca gctggaaat gttgccagag gaataaacat tgccattgtc 350
aactatgtaa ctgggaatgt gacagcaaca cgtatgtttg atatgtatga 400
aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

aacgatgcc aagaatgccat agaagcactt ggaagtaaag aaatcaggaa 550
catgaaattc aggtctagct gggtatttat tgcagcaaaa ggcttggAAC 600
tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650
aacagatatt ctggctggcc tgcagagatc cagatagaag gctgcataacc 700
caaagaacga agctgacact gcagggtcct gagtaatgt gttctgtata 750
aacaaatgca gctggaatcg ctcaagaatc ttatTTTct aaatccaaca 800
gccccatattt gatgagtatt ttgggTTTgt tggaaaccaa tgaacatttg 850
ctagttgtat caaatcttgg tacgcagtat ttttatacca gtatTTTatg 900
tagtgaagat gtcaatttgc agggaaactaa aatgaatgga aattcttaaa 950
aaaaaaaa 957

<210> 91
<211> 235
<212> PRT
<213> Homo Sapien

<400> 91
Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
1 5 10 15
Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
20 25 30
Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
35 40 45
Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
50 55 60
Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
65 70 75
Tyr Arg Leu Leu Ser Gly Gly Arg Ser Lys Tyr Ala Lys Ile
80 85 90
Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
95 100 105
Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
110 115 120
Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
125 130 135
Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
140 145 150
Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180
Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195
Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
200 205 210
Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
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